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Figure 1: Top ten NCBI non redundant protein database hits for INSP081.

BLASTP 2.2.2 [Jan-08-2002]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= INSP081.pep
(1132 letters)

Database: ncbi-nr
1,039,718 sequences; 328,277,582 total letters

Searching.....done

	Score (bits)	E Value
Sequences producing significant alignments:		
dbj BAA87066.1 (AB035267) Nck-interacting kinase-like embryo sp...	1223	0.0
ref NP_038752.1 (NM_013724) Nik related kinase [Mus musculus] >...	1220	0.0
ref XP_125446.1 (XM_125446) similar to Nck-interacting kinase-l...	1160	0.0
ref XP_109557.1 (XM_109557) similar to Nik related kinase [Mus ...	747	0.0
ref NP_004825.1 (NM_004834) mitogen-activated protein kinase ki...	393	e-108
gb AAF03788.1 AF172270_1 (AF172270) Traf2 and NCK interacting ki...	392	e-107
gb AAF03786.1 AF172268_1 (AF172268) Traf2 and NCK interacting ki...	392	e-107
gb AAF03789.1 AF172271_1 (AF172271) Traf2 and NCK interacting ki...	392	e-107
gb AAF03785.1 AF172267_1 (AF172267) Traf2 and NCK interacting ki...	392	e-107
dbj BAA25477.2 (AB011123) KIAA0551 protein [Homo sapiens]	392	e-107
gb AAF03783.1 AF172265_1 (AF172265) Traf2 and NCK interacting ki...	392	e-107
gb AAF03782.1 AF172264_1 (AF172264) Traf2 and NCK interacting ki...	392	e-107
gb AAF03787.1 AF172269_1 (AF172269) Traf2 and NCK interacting ki...	392	e-107

Figure 2: INSP081 top blastp alignment result from NCBI non-redundant protein database sequences.

>dbj|BAA87066.1| (AB035267) Nck-interacting kinase-like embryo specific kinase [Mus musculus]
Length = 1455

Score = 1223 bits (3165), Expect = 0.0

Identities = 669/1154 (57%), Positives = 760/1154 (64%), Gaps = 47/1154 (4%)

Query: 1 MAGPGGWRDREVTDLGHLDPDTGIFSLDKTIGLGTYGRIYGLHEKTGAFTAVKVMNARK 60
MAGPG WRD+EVTDLG LPDPTGIFSLDK IGLGTYGRI+LG+HEKTG+ AVKVM+ARK
Sbjct: 1 MAGPGSWRDKEVTDLGQLPDTGIFSLDKAIGLGTYGRIFLGIHEKTGSLVAVKVMARK 60

Query: 61 TPLPEIGRRVRVVKYQKSVGWRYSDDEEDLRTELNLLRKYSFHKNIVSFYGAFFKLSPPG 120
TPLPEIGRRVRVVKYQKSVGWRYSDDEEDLRTELNLLRKYSFHKNIIV+FYGAFFKL+PPG
Sbjct: 61 TPLPEIGRRVRVVKYQKSVGWRYSDDEEDLRTELNLLRKYSFHKNIIVTFYGAFFKLNP 120

Query: 121 QRHQLWMVMELCAAGSVTDVVRMTSNQSLKEDWIAIYICREILQGLAHLHAHVIHRDIK 180
+HQLWMVMELCAAGSVTDVVRMT NQSLKEDWIAIYICREILQGLAHLHAH+VIHRDIK
Sbjct: 121 QRHQLWMVMELCAAGSVTDVVRMTNQLKEDWIAIYICREILQGLAHLHAHVIHRDIK 180

Query: 181 QNVLLTHNAEVKLVDFGVSAQVSRTNGRRNSFIGTPYWMapeVIDCDEDPRRSYDYRSDV 240
QNVLLTH+AEVK+VDFGVSAQVSRTNGRRNSFIGTPYWMapeVI CDEDPR SYDYRSDV
Sbjct: 181 QNVLLTHDAEVKLVDFGVSAQVSRTNGRRNSFIGTPYWMapeVIHCDEDPRCSYDYRSDV 240

Query: 241 WSVGITAIEAEGAPPLCNLQPLEALFVILRESAPT VKSSGWSRKFNFMKCTIKNLF 300
WSVGITAIEAEGAPPLC LQPLEAL VILRE+AP VKSSGWSRKFNFME C IKNLF
Sbjct: 241 WSVGITAIEAEGAPPLCKLQPLEALCVILREAPVKSSGWSRKFNFMENCMIKNLF 300

Query: 301 RPTSANMLQHPFVRDIKNERHVESLTRLHTGIIKKRQKKGIPLIFEREEAIKEQYTVRR 360
RPTS NML HPFV DIKNER VVESLT+HLTGII+KR+KKGIP+ FE EEA KEQY RR
Sbjct: 301 RPTSGNMLLHPFVHDIKNERRVESLTKHLTGIIQKREKGIPLVAFEGEEAAKEQYITR 360

Query: 361 FRGPSCTHELLRLPTSSRCRPLRVLHGEPSPQRWLPDREEPXXXXXXXXXXXXRVFMPLQ 420
FRGPSCT ELLR+PTSSRCRPLRVLHGEP QPRWLPD+E+P VFMP
Sbjct: 361 FRGPSCTPELLRVPTSSRCRPLRVLHGEPQPRWLPDQEDPQDELQQLQKAAGVFMPLH 420

Query: 421 ALDSAPKPLKGQAQAPQRLQGAARVFMPLQAQVKAKASKPLQMQUIXXXXXXXXXXXXX 480
+ D+ K Q + L+GAA+V MP+ QV+A P Q+
Sbjct: 421 SQDNTSKLFPKQVEVAPYLRGAAQVVMPLVQVEA----PPQVSKAAQMLRSLPTQDNKA 476

Query: 481 XQAQVRAPRLXXXXXXXXXXXXXXXXXSEPQDLQVPEEFQGGDQVXXXXXXXXXXXXX 540
+V+AP +P+DLQVPEEFQGGD+
Sbjct: 477 TSPEVQAP-----VAEGQQAQHEALETEQPKDLQVPEEFQGGDRAPEQPRQGAAEQ 531

Query: 541 XHNQVPEQELXXXXXXXXXXXXXXXXXXXXXXXXXSLRVNAQVFLPLLSQDHHVLL 600
HN VPEQ ++V+AQV LPLLSQ+ HVLL
Sbjct: 532 IHNVPVEQPPEEDREPEQAEVQEEAVEPPQAEIEDKEPEVVQVHAQVLLPLLSQNRHVLL 591

Query: 601 PLHLDQVLPVGEQTEGSPQAQAWTLEPPQAIGSVQALIEGLSRDLLRAPNSNNSKPLG 660
PLHLD Q+LIPV Q E P+AQAW LE +A+G+VQALIEGLSRDLLRAPN+ +KPLG
Sbjct: 592 PLHLDRLQVLPVGEQNEEVPRQAQAWDLEASRAVGAVQALIEGLSRDLLRAPNAFVTKPLG 651

Query: 661 PLQTLMENLSSNRFYSQPEQAREKSKVSTLRQALAKRLSPKRFRKSSWRPEKLESD 720
PLQ +ENLS++ FY++PE ++KSKV++LR+A+AKRL PKRFRK+ WR E E SD+
Sbjct: 652 PLQIFLENLSTDGFTYPEPTQKKKSKVASLRKAIAKRLPKRFRKALWLEDFEFS 711

Query: 721 EAXXXXXXXXXXWEDIFNQHEELRQVXXXXXXXXXXXXXVFHSIQAEVQIEPLKPYISNPK 780
E WEDIFNQHEE+LR+V VFHSIQAEVQIE P+ +NP
Sbjct: 712 ETSRRRRHRRWEDIFNQHEELRRVENDREDDSSDNDEVFHSIQAEVQIE---PHANPA 768

Query: 781 KIEVQERSPSVPNNQDHAHVKFSSRTWHMLFCLFTISVPQRSLLAQKPIDIRQSSQN 840
EV ERS +P N++ H VKFS L + PQ +Q Q+P++IR R+ N
Sbjct: 769 GNEVHERSAPMPCNRNRTHRVKFSPSVGEESPLEEAQPQ----QQQQPMNIRPRNCLN 824

Query: 841 RQNWLAAXXXXXXXXXXPVTGRRSQSSPPYSTIDQKLLVDIHVPDGFVKVGKISPPVYLTNE 900
QN+ A PVT R+SQSSPPYSTIDQKLL+DIHVPDGFVKVGKISPPVYLTNE
Sbjct: 825 PQNFQAQSDSSSEEDSPVTRRKSQSSPPYSTIDQKLLIDIHVPDGFVKVGKISPPVYLTNE 884

Query: 901 WVGYNALSEIFRNDWLTPAPVIQPPEEDGDYVELYXXXXXXXXXXXXXXXXXXTYDHA 960
WVGYNALSEIF +DW+ P +PPEEDGDYVELY D A
Sbjct: 885 WVGYNALSEIFWDDWIMPTRPARPPEEDGDYVELY-DADANANGDEEVANGAYEDPRDGA 943

Query: 961 NGNDDLDNQVDQANDVCXXXXXXXXXXXXXXXXXXYEAPSCPRASYGRDGSCQDGYDGS 1020
NG+DD++NQ+DQAN + A + PRA+Y R G K DG
Sbjct: 944 NGHDDMNNQLDQANG--YEGHGAAGYNGGDVGGNHGAAGFNGPRANYPRAGILKNHNDGR 1001

Query: 1021 RGKEEAYRGYSHTANRSHGGSAAASEDNAAIGDQEEHAANXXXXXXXXXXXXXXXXXNEASN 1080
A+ +G + A HG AA E AA G+ H AN NE +
Sbjct: 1002 ALNRGAFGVFGDNAAARAFHG--AAGEAGAAFGN--HGANRGNGRGNRNRREANGRNEENG 1056

Query: 1081 AI--DSGAAPSAPDHESD-----NKDISESSTQSDFSANHSPPSK 1118
A D P ESD N SST F SSP +
Sbjct: 1057 AFGRDQHVFPEFEHEESDRGTETSDSIALEITSFDGEQNSGRPVSSTTMGFPIGRSSP-R 1115

Query: 1119 GSGMSADANFASAI 1132
GS +D ++ S I
Sbjct: 1116 GSDFGSDISYNSPI 1129

Figure 3: Top ten NCBI non redundant protein database hits for INSP082.

BLASTP 2.2.2 [Jan-08-2002]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= chrX_101702493-101913965_hg11.pep
(1500 letters)

Database: ncbi-nr
1,039,718 sequences; 328,277,582 total letters

Searching.....done

Sequences producing significant alignments:	Score (bits)	E Value
dbj BAA87066.1 (AB035267) Nck-interacting kinase-like embryo sp...	1727	0.0
ref NP_038752.1 (NM_013724) Nik related kinase [Mus musculus] >...	1724	0.0
ref XP_125446.1 (XM_125446) similar to Nck-interacting kinase-l...	1664	0.0
ref XP_109557.1 (XM_109557) similar to Nik related kinase [Mus ...	1251	0.0
emb CAB06091.1 (Z83850) mouse NIK serine threonine protein kina...	599	e-170
ref NP_004825.1 (NM_004834) mitogen-activated protein kinase ki...	393	e-108
gb AAF03788.1 AF172270_1 (AF172270) Traf2 and NCK interacting ki...	392	e-107
gb AAF03786.1 AF172268_1 (AF172268) Traf2 and NCK interacting ki...	392	e-107
gb AAF03789.1 AF172271_1 (AF172271) Traf2 and NCK interacting ki...	392	e-107
gb AAF03785.1 AF172267_1 (AF172267) Traf2 and NCK interacting ki...	392	e-107
dbj BAA25477.2 (AB011123) KIAA0551 protein [Homo sapiens]	392	e-107
gb AAF03783.1 AF172265_1 (AF172265) Traf2 and NCK interacting ki...	392	e-107

Figure 4: INSP082 top blastp alignment result from NCBI non-redundant protein database sequences.

>dbj|BAA87066.1| (AB035267) Nck-interacting kinase-like embryo specific kinase [Mus musculus]
Length = 1455

Score = 1727 bits (4473), Expect = 0.0

Identities = 923/1505 (61%), Positives = 1058/1505 (69%), Gaps = 55/1505 (3%)

```

Query: 1      MAGPGGWRDREVTDLGHLPDPTGIFSLDKTIGLGTYGRIYGLHEKTGAFTAVKVMNARK 60
             MAGPG WRD+EVTDLG LPDPTGIFSLDK IGLGTYGRI+LG+HEKTG+ AVKVM+ARK
Sbjct: 1      MAGPGSWRDKEVTDLGQLPDPTGIFSLDKAIGLGTYGRIFLGIHEKTGSLVAVKVMNARK 60

Query: 61     TPLPEIGRRVRVNKYQKSVGWRYSDDEEDLRTELNLLRKYSFHKNIVSFYGAFFKLSPPG 120
             TPLPEIGRRVRVNKYQKSVGWRYSDDEEDLRTELNLLRKYSFHKNIIV+FYGAFFKL+PPG
Sbjct: 61     TPLPEIGRRVRVNKYQKSVGWRYSDDEEDLRTELNLLRKYSFHKNIIVTFYGAFFKLNP 120

Query: 121    QRHQLWMVMELCAAGSVTDVVRMTSNQSLKEDWIAYICREILQGLAHLHAHVIHRDIK 180
             +HQLWMVMELCAAGSVTDVVRMT NQSLKEDWIAYICREILQGLAHLHAH+VIHRDIK
Sbjct: 121    HQHQLWMVMELCAAGSVTDVVRMTNRNQLKEDWIAYICREILQGLAHLHAHQVIHRDIK 180

Query: 181    QNVLLTHNAEVKLVDGVSQAQVSRRTNGRRNSFIGTPYWMAPEVIDCDEDPRRSYDYRSDV 240
             QNVLLTH+AEVK+VDFGVSAQVSRRTNGRRNSFIGTPYWMAPEVI CDEDP SYDYRSDV
Sbjct: 181    QNVLLTHDAEVKIVDFGVSAQVSRRTNGRRNSFIGTPYWMAPEVIHCDEDP RSYDYRSDV 240

Query: 241    WSVGITAIEAEGAPPLCNLQPLEALFVILRESAPT VKSSGWSRKFNHFMKCTIKNFLF 300
             WSVGITAIEAEGAPPLC LQPLEAL VILRE+AP VKSSGWSRK FNME C IKNFLF
Sbjct: 241    WSVGITAIEAEGAPPLCKLQPLEALCVILREAAPVKSSGWSRKFNHFMENCMIKNFLF 300

Query: 301    RPTSANMLQHPFVRDIKNERHVESLTRHLTGIIKKRQKGIPLIFEREEAIKEQYTVRR 360
             RPTS NML HPFV DIKNER VVESLT+HLTGII+KR+KKGIP+ FE EEA KEQY RR
Sbjct: 301    RPTSGNMLLHPFVHDIKNERRVVESLTKHLTGIIQKREKGIPIVAFEGEEAAKEQYITRR 360

Query: 361    FRGPSCTHELLRLPTSSRCRPLRVLHGEPSQPRWLPDREEPXXXXXXXXXXXXXVFEMPLQ 420
             FRGPSCT ELLR+PTSSRCRPLRVLHGE PPRWLPD+E+P VFEMPL
Sbjct: 361    FRGPSCTPELLRVPTSSRCRPLRVLHGEPPQPRWLPDQEDPDQDQELQQLQKAAGVFEMPLH 420

Query: 421    ALDSAPKPLKGQAQAPQRLQGAARVFMPLQAQVKAKASKPLQMQIKXXXXXXXXXXXXX 480
             + D+ K Q + L+GAA+V MP+ QV+A P Q+
Sbjct: 421    SQDNTSKLFQKQVEVAPYLRGAAQVMPVLVQVEA----PPQVSKAAQMLRSLPTQDNKA 476

Query: 481    XQAQVRAPRLXXXXXXXXXXXXXXXXXSEPDLDQVPEEFQGGDQVXXXXXXXXXXXXX 540
             +V+AP +P+DLDQVPEEFQGGD+
Sbjct: 477    TSPEVQAP-----VAEGQQAQHEALETEQPKDLQVPEEFQGGDRAPEQPRQGAAEQQQ 531

Query: 541    XHNQVPEQELXXXXXXXXXXXXXXXXXXXXXXXXXSLRVNAQVFLPLLSQDHHVLL 600
             HN VPEQ ++V+AQV LPLLSQ+ HVLL
Sbjct: 532    IHNVPVPEQPPEEDREPEQAEVQEEAVEPPQAEIEDKEPEVVQVHAQVLLPLLSQNRHVLL 591

Query: 601    PLHLDQTQVLIPVEGQTEGSPQAQAWTLEPPQAIGSVQALIEGLSRDLLRAPNSNNSKPLG 660
             PLHLD Q+LIPV Q E P+AQAW LE +A+G+VQALIEGLSRDLLRAPN+ +KPLG
Sbjct: 592    PLHLDRLQLLIPVGEQNEEVPRQAQAWLEASRAVGAVQALIEGLSRDLLRAPNAFVTKPLG 651

Query: 661    PLQTLMENLSSNRFYSQPEQAREKKSVSTLRQALAKRLSPKRFRAKSSWRPEKLELSDL 720
             PLQ +ENLS++ FY++PE ++KSKV++LR+A+AKRL PKRFRAK+ WR E E SD+
Sbjct: 652    PLQIFLENLSTDGFYTEPEPTQKKKSVASLRKAIKRLRPKRFRAKALWRLEDFEFSDV 711

Query: 721    EAXXXXXXXXXWEDIFNQHEELRQVXXXXXXXXXXXXXVFHSIQAEVQIEPLKPYISNPK 780
             E WEDIFNQHEE+LR+V VFHSIQAEVQIE P+ +NP
Sbjct: 712    ETSRRRRHRRWEDIFNQHEELRRVENDREDDSSDNDEVFHSIQAEVQIE---PHAANPA 768

Query: 781    KIEVQERSPSVPNNQDHAHVKFSSRTWHMLFCLFISVPQRSLLQEAQKPIDIRQSSQN 840
             EV ERS +P N++ H VKFS L + PQ +Q Q+P++IR R+ N
Sbjct: 769    GNEVHERSAPMPCNRNRTHRVKFSVSGEEPSLEEAPQ-----QQQQPMNIRPRNCLN 824

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Query: 841 RQNWLAAXXXXXXXXXXVPTGRRSQSSPPYSTIDQKLLVDIHVPDGFVKVKGISPPVYLTNE 900
QN+ A PVT R+SQSSPPYSTIDQKLL+DIHVPDGFVKVKGISPPVYLTNE
Sbjct: 825 PQNFQAQSDSSSEEDSPVTRRKSQSSPPYSTIDQKLLIDIHVPDGFVKVKGISPPVYLTNE 884

Query: 901 WVGYNALSEIFRNDWLTAPVIQPPEDGDYVELYXXXXXXXXXXXXXXXXXXXXTYDHA 960
WVGYNALSEIF +DW+ P +PPEEDGDYVELY D A
Sbjct: 885 WVGYNALSEIFWDDWIMPTRPARPPEEDGDYVELY--DADANANGDEEVANGAYEDPRDGA 943

Query: 961 NGNDDLDNQVDQANDVCXXXXXXXXXXXXXXXXXXYEAPSCPRASYGRDGSCKQDGYDGS 1020
NG+DD++NQ+DQAN + A + PRA+Y R G K DG
Sbjct: 944 NGHDDMNNQLDQANG--YEGHGAAGYNGGDVGGNHGAAFNPRANYPRAGILKNHNDGR 1001

Query: 1021 RGKEEAYRGYGSHTANRSHGSSAASEDNAAIGDQEEHAANXXXXXXXXXXXXXXXXXNEASN 1080
A+ +G + A HG AA E AA G+ H AN NE +
Sbjct: 1002 ALNRGAFGVFGDNAAARAFHG--AAGEAGAAFGN---HGANRGNRGRNRNREANGRNEENG 1056

Query: 1081 AI--DSGAAPSAPDHESDNKDISESTQSDFSANHSSPSKSGSGMSADANFASAILYAGFV 1138
A D P ESD + S + ++ + G +S+ GF
Sbjct: 1057 AFGRDQHVFEFEHEESDRGTETSDSIALEITSFDGEQNSGRFVSST-----MGF- 1107

Query: 1139 EVPEESPQKP---SEVNVNPLYVSPACKKPLIHMYEKEFTSEICGSLWGVNLLLGTRSN 1195
+ SP+ S+++ N P++H+YEK+F+SE+ CGSLWGVNLLLGTS+
Sbjct: 1108 PIGRSSPRGSDFGSDISYN-----SPILVHYEKDFSSEVYCGSLWGVNLLLGTSQSH 1158

Query: 1196 LYLMDRSGKADITKLIIRRRPFRQIQVLEPLNLLITISGHKNRLRVYHLTWLRNKILNNDP 1255
LYLMDRSGKA+I KLI+RRPFRQIQV+E LNLLITISG KNRLRVYHL+WLRNKILNNDP
Sbjct: 1159 LYLMDRSGKAEIVKLIKRRPFRQIQVVEQLNLLITISGKNRLRVYHLSWLRNKILNNDP 1218

Query: 1256 ESKRRQEEMLKTEEACKAIDKLTGCEHFSVLQHEETTYIAIALKSSIHLYAWAPKSFDES 1315
+SK+RQ+ M K EEACKAIDKL GCEHFSVLQHEETTYIA+A+KSSIHL+AWAPKSFDE+
Sbjct: 1219 KSKKRQKAMRKKEEACKAIDKLIGCEHFSVLQHEETTYIAVAVKSSIHLEFAWAPKSFDEN 1278

Query: 1316 TAIKVFPPTLDHKPVTVDLAIGSEKRLKIFFSSADGYHLIDAESEVMSDVTLPKXXXXXXX 1375
TAIKVFPT D KP+TVDLA+GSEK LKIFFSSA+GYH+IDAESEVMS+VTLP
Sbjct: 1279 TAIKVFPTRDLKPLTVDLAVGSEKTLKIFFSSANGYHIIDAESEVMSEVTLPN----- 1331

Query: 1376 XXXXXXXXDCLGIGMMLTFNAEALSVEANEQLFKKILEMWKDIPSSIAFECTQRTTGWGQ 1435
DCLG+G+ML+ NAEA S EANEQL KKIL++WKDIPSS+AFECT+R TGW Q
Sbjct: 1332 -NNVVILPDCLGLGVMLSLNAEAAEEANEQLKKILDVWKDIPSSVAFECTKRITGWDQ 1390

Query: 1436 KAIEVRSLSQSRVLESELKRRSIKKLRLCTRGDKLFFTSTLRNHHSRVYFMTLGKLEELQ 1495
KAIEVRSLSQ +LE+ELKRRSIKKLRLC RGDK+FF STL N HSRVY M+LGKLEEL
Sbjct: 1391 KAIEVRSLSQSTILENELKRRSIKKLRLCARGDKMFFASTLSNDHSRVYLSLGLKLEELH 1450

Query: 1496 SNYDV 1500
+Y V
Sbjct: 1451 RSYAV 1455

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Figure 5: Top ten NCBI non redundant protein database hits for INSP082.

BLASTP 2.2.2 [Jan-08-2002]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= genomic.pep
(1589 letters)

Database: ncbi-nr
1,039,718 sequences; 328,277,582 total letters

Sequences producing significant alignments:	Score (bits)	E Value
dbj BAA87066.1 (AB035267) Nck-interacting kinase-like embryo sp...	1708	0.0
ref NP_038752.1 (NM_013724) Nik related kinase [Mus musculus] >...	1704	0.0
ref XP_109557.1 (XM_109557) similar to Nik related kinase [Mus ...	1232	0.0
ref XP_125446.1 (XM_125446) similar to Nck-interacting kinase-l...	1048	0.0
emb CAB06091.1 (Z83850) mouse NIK serine threonine protein kina...	599	e-170
ref NP_004825.1 (NM_004834) mitogen-activated protein kinase ki...	393	e-108
gb AAF03788.1 AF172270_1 (AF172270) Traf2 and NCK interacting ki...	392	e-107
gb AAF03786.1 AF172268_1 (AF172268) Traf2 and NCK interacting ki...	392	e-107
gb AAF03789.1 AF172271_1 (AF172271) Traf2 and NCK interacting ki...	392	e-107
gb AAF03785.1 AF172267_1 (AF172267) Traf2 and NCK interacting ki...	392	e-107
dbj BAA25477.2 (AB011123) KIAA0551 protein [Homo sapiens]	392	e-107

Figure 6: INSP091 top blastp alignment result from NCBI non-redundant protein database sequences.

>dbj|BAA87066.1| (AB035267) Nck-interacting kinase-like embryo specific kinase [Mus musculus]
Length = 1455

Score = 1708 bits (4423), Expect = 0.0

Identities = 935/1590 (58%), Positives = 1070/1590 (66%), Gaps = 136/1590 (8%)

```

Query: 1      MAGPGGWRDREVTDLGHLDPDTGIFSLDKTIGLGTYGRIYGLGHEKTGAFTAVKVMNARK 60
              MAGPG WRD+EVTDLG LPDPTGIFSLDK IGLGTYGRI+LG+HEKTG+ AVKVM+ARK
Sbjct: 1      MAGPGSWRDKEVTDLGQLPDTGIFSLDKAIGLGTYGRIFLGIHEKTGSLVAVKVMARK 60

Query: 61     TPLPEIGRRVRVKNYQKSVGWRYSDDEEDLRTELNLLRKYSFHKNIVSFYGAFFKLSPPG 120
              TPLPEIGRRVRVKNYQKSVGWRYSDDEEDLRTELNLLRKYSFHKNIIV+FYGAFFKL+PPG
Sbjct: 61     TPLPEIGRRVRVKNYQKSVGWRYSDDEEDLRTELNLLRKYSFHKNIIVTFYGAFFKLNP 120

Query: 121    QRHQLWMVMELCAAGSVTDVVRMTSNQSLKEDWIAYICREILQGLAHLHAHRVHRDIK 180
              +HQLWMVMELCAAGSVTDVVRMT NQSLKEDWIAYICREILQGLAHLHAH+VIHRDIK
Sbjct: 121    HQHQLWMVMELCAAGSVTDVVRMTNRNQLKEDWIAYICREILQGLAHLHAHQVIHRDIK 180

Query: 181    QNVLLTHNAEVKLVDFGVSAQVSRNNGRRNSFIGTPYWMapeVIDCEDPRRSYDYSRV 240
              QNVLLTH+AEVK+VDFGVSAQVSRNNGRRNSFIGTPYWMapeVI CDEDP SYDYSRV
Sbjct: 181    QNVLLTHDAEVKLVDFGVSAQVSRNNGRRNSFIGTPYWMapeVIHCDEDPSCSYDYSRV 240

Query: 241    WSVGITAEMAEGAPPLCNLQPLEALFVILRESAPTVKSSGWSRKFNHFMKCTIKNFLF 300
              WSVGITAEMAEGAPPLC LQPLEAL VILRE+AP VKSSGWSRKFNME C IKNFLF
Sbjct: 241    WSVGITAEMAEGAPPLCKLQPLEALCVILREAAAPKVKSSGWSRKFNFMENCMIKNFLF 300

Query: 301    RPTSANMLQHPFVRDIKNERHVVESLTRHLTGIIKKRQKKGIPLIFEREAAIKEQYTVRR 360
              RPTS NML HPFV DIKNER VVESLT+HLTGII+KR+KKGIP+ FE EEA KEQY RR
Sbjct: 301    RPTSGNMLLHPFVHDIKNERRVVESLT+KHLTGIIQKREKKGIPVAFEGEEAAKEQYITRR 360

Query: 361    FRGPSCTHELLRLPTSSRCRPLRVLHGEPSPQRWLPDREEPXXXXXXXXXXXXXRVFMPLQ 420
              FRGPSCT ELLR+PTSSRCRPLRVLHGEP QPRWLPD+E+P VFMPL
Sbjct: 361    FRGPSCTPELLRVPTSSRCRPLRVLHGEPQPRWLPDQEDPDQELQQLQKAGVFMPLH 420

Query: 421    ALDSAPKPLKGQAQAPQRLQGAARVFMPLQAVKAKASKPLQMQUIXXXXXXXXXXXXX 480
              + D+ K Q + L+GAA+V MP+ QV+A P Q+
Sbjct: 421    SQDNTSKLFPKQVEVAPYLRGAAQVMPVLVQVEA----PPQVSKAAQMLRSLPTQDNKA 476

Query: 481    XQAQVRAPRLXXXXXXXXXXXXXXXXXSEPDLDQVPPEFQGDQVXXXXXXXXXXXXX 540
              +V+AP +P+DLDQVPPEFQGD+
Sbjct: 477    TSEVQAP-----VAEQQAQHEALETEQPKDLDQVPPEFQGDRAPEQPRQGAAEQQQ 531

Query: 541    XHNQVPEQELXXXXXXXXXXXXXXXXXXXXXXXXXXXXSLRVNAQVFLPLLSQDHHVLL 600
              HN VPEQ ++V+AQV LPLLSQ+ HVLL
Sbjct: 532    IHNVPVEQPPEEDREPEQAQEVQEEAVEPPQAETEDKEPEVVQVHAQVLLPLLSQNRHVLL 591

Query: 601    PLHLDQVLIPVEGQTEGSPQAQAWTLEPPQAIGSVQALIEGLSRDLLRAPNSNNSKPLG 660
              PLHLD Q+LIPV Q E P+AQAW LE +A+G+VQALIEGLSRDLLRAPN+ +KPLG
Sbjct: 592    PLHLDRLQVLIPVEGQNEEVPRQAQWLEASRAVGAVQALIEGLSRDLLRAPNAFVTKPLG 651

Query: 661    PLQTLMENLSSNRFYSPQEQAREKSKVSTLRQALAKRLSPKRFRAKSSWRPEKLELSDL 720
              PLQ +ENLS++ FY++PE ++KSKV++LR+A+AKRL PKRFRAK+ WR E E SD+
Sbjct: 652    PLQIFLENLSTDGFTTEPTQKKSKVASLRKAIAKRLRPKRFRAKALWRLEDFEFSDV 711

Query: 721    EAXXXXXXXXXXWEDIFNQHEELRQVXXXXXXXXXXXXXVFHSIQAEVQIEPLKPYISNPK 780
              E WEDIFNQHEE+LR+V VFHSIQAEVQIEP + +NP
Sbjct: 712    ETSRRRRHRRWEDIFNQHEELRRVENDREDDSSDNDEVFHSIQAEVQIEP---HAANPA 768

Query: 781    KIEVQERSPSVPNNQDHAHHVKFSSSVQRS-LLEQAQKPIDIRQRSSQNRQNLAAAGSD 839
              EV ERS +P N++ H VKFS SV + LE+AQ
Sbjct: 769    GNEVHERSAPMPCNRRNRTHRVKFSVSGVEEPSLEEAQP----- 807

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Query: 840 SKHKILAGKTQSYCLTIYISEVKKEEFQEGMNQKCQGAQVGLGPEGHCWQLGESSSEEE 899
+++ Q+ MN + + L P+ +SSSE+
Sbjct: 808 -----QQQQQPMNIRPRNC---LNPQN---FQAQSDSSSEED 839

Query: 900 SPVTGRRSQSSPPYSTIDQKLLVDIHVPDGFVKVGI SPPVYL TNEWVGYNALSEIFRNDW 959
SPVT R+SQSSPPYSTIDQKLL+DIHVPDGFVKVGI SPPVYL TNEWVGYNALSEIF +DW
Sbjct: 840 SPVTRRKSQSSPPYSTIDQKLLIDIHVPDGFVKVGI SPPVYL TNEWVGYNALSEIFWDDW 899

Query: 960 LTPAPVIQPEEDGDYVELYXXXXXXXXXXXXXXXXXXXXTYDHANGNDDLNDQVDQAND 1019
+ P +PPEEDGDYVELY D ANG+DD++NQ+DQAN
Sbjct: 900 IMPTRPARPPEEDGDYVELYDADANANGDEEVANGAYEDPR-DGANGHDDMNQLDQANG 958

Query: 1020 VCXXXXXXXXXXXXXXXXXXYYEAPSCPRASYGRDGSKQDGYDGSRGKEEAYRGYSHTA 1079
+ A + PRA+Y R G K DG A+ +G + A
Sbjct: 959 Y--EGHGAAGYNGGDVGGNHGAAFNGPRANYPRAGILKNHNDGRALNRGAFGVFGDNAA 1016

Query: 1080 NRSHGSSAASEDNAAIGDQEEHAANIXXXXXXXXXXXXXXVVRTSEESGALGLNGEENC 1139
HG AA E AA G+ H AN +G N E N
Sbjct: 1017 RAFHG--AAGEAGAAFGN---HGAN-----RGNGRGNRNREANGR 1051

Query: 1140 ETDGPGLRKPASQDFEYLQEEPPGGGNEASNAIDSGAAPSAPDHESDNKDISESSTQSDFS 1199
+ R E+ EE G E S++I A N SST F
Sbjct: 1052 NEENGAFGRDQHVFPFEFEHEESDRGTETSDSI---ALEITSFDGEQNSGRPVSSSTMGFP 1108

Query: 1200 ANHSSPSKSGSMSADANFASAILYAGFEVPEESPKQFSEVNPNPLYVSPACKKPLIHMY 1259
SSP +GS +D ++ S P++H+Y
Sbjct: 1109 IGRSSP-RGSDFGSDISYNS-----PILHVV 1133

Query: 1260 EKEFTSEICGSLWGVNLLLGTSLNLYLMDRSGKADITKLIRRRPFRQIQVLEPLNLLIT 1319
EK+F+SE+ CGSLWGVNLLLGT+S+LYLMDRSGKA+I KLI+RRPFRQIQV+E LNLLIT
Sbjct: 1134 EKDFSSEVYCGSLWGVNLLLGTQSHLYLMDRSGKAEIVKLIKRRPFRQIQVVEQLNLLIT 1193

Query: 1320 ISGHKNRLRVYHLTWLRNKILNNDPESKRRQEEMLKTEEACKAIDKLTGCEHFSVLQHEE 1379
ISG KNRLRVYHL+WLRNKILNNDP+SK+RQ+ M K EEACKAIDKL GCEHFSVLQHEE
Sbjct: 1194 ISGKNRLRVYHLSWLRNKILNNDPKSKKRQKAMRKKEEACKAIDKLIGCEHFSVLQHEE 1253

Query: 1380 TTYIAIALKSSIHLYAWAPKSFDESTAIKVFPPTLDHKPVTVDLAIGSEKRLKIFFSSADG 1439
TTYIA+A+KSSIHL+AWAPKSFDE+TAIKVFPT D KP+TVDLA+GSEK LKIFFSSA+G
Sbjct: 1254 TTYIAVAVKSSIHFAWAPKSFDETAIKVFPTRDLPKPLTVDLAVGSEKTLKIFFSSANG 1313

Query: 1440 YHLIDAESEVMSDVTLPKXXXXXXXXXXXXXDCLGIGMMLTFNAEALSVEANEQLFKK 1499
YH+IDAESVMS+VTLP DCLG+G+ML+ NAEA S EANEQL KK
Sbjct: 1314 YHIIDAESEVMSEVTLPN-----NNVVILPDCLGLGVMLSLNAEAAESEANEQLLKK 1365

Query: 1500 ILEMWKDIPSSIAFECTORTTGWGQKAIEVRSLSRVLESELKRRSIKKLRFLCTRGDKL 1559
IL++WKDIPSS+AFECT+R TGW QKAIEVRSLS +LE+ELKRRSIKKLRFLC RGDK+
Sbjct: 1366 ILDVWKDIPSSVAFECTKRITGWDQKAIEVRSLSQSTILENELKRRSIKKLRFLCARGDKM 1425

Query: 1560 FFTSTLRNHHSRVYFMTLGKLEELQSNYDV 1589
FF STL N HSRVY M+LGKLEEL +Y V
Sbjct: 1426 FFASTLSNDHSRVYMLSLGKLEELHRSYAV 1455

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Figure 7: CLUSTAL alignment of INSP081, 082, 091 & published ZC4 coding sequences.

*** = kinase domain

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ZC4      MAGPGGWRDREVTDLGHLDPDPTGIFSLDKTIGLGTYGRIYGLHEKTGAFTAVKVMNARK
INSP081  MAGPGGWRDREVTDLGHLDPDPTGIFSLDKTIGLGTYGRIYGLHEKTGAFTAVKVMNARK
INSP082  MAGPGGWRDREVTDLGHLDPDPTGIFSLDKTIGLGTYGRIYGLHEKTGAFTAVKVMNARK
INSP091  MAGPGGWRDREVTDLGHLDPDPTGIFSLDKTIGLGTYGRIYGLHEKTGAFTAVKVMNARK
*****

ZC4      -----DEEDLRTELNLLRKYSFHKNIVSFYGAFFKLSPPG
INSP081  TPLPEIGRRVRVVKYQKSVGWRYSDEEDLRTELNLLRKYSFHKNIVSFYGAFFKLSPPG
INSP082  TPLPEIGRRVRVVKYQKSVGWRYSDEEDLRTELNLLRKYSFHKNIVSFYGAFFKLSPPG
INSP091  TPLPEIGRRVRVVKYQKSVGWRYSDEEDLRTELNLLRKYSFHKNIVSFYGAFFKLSPPG
*****
          CP3 →

ZC4      QRHQLWVMELCAAGSVTDVVRMTSNQSLKEDWIAYICREILQGLAHLHAHRVHRDIKG
INSP081  QRHQLWVMELCAAGSVTDVVRMTSNQSLKEDWIAYICREILQGLAHLHAHRVHRDIKG
INSP082  QRHQLWVMELCAAGSVTDVVRMTSNQSLKEDWIAYICREILQGLAHLHAHRVHRDIKG
INSP091  QRHQLWVMELCAAGSVTDVVRMTSNQSLKEDWIAYICREILQGLAHLHAHRVHRDIKG
*****
                                     ← CP4

ZC4      QNVLLTHNAEVKLVDGVSQAQVSRNTNGRRNSFIGTPYWMAPEVIDCDEDPRRSYDYSRV
INSP081  QNVLLTHNAEVKLVDGVSQAQVSRNTNGRRNSFIGTPYWMAPEVIDCDEDPRRSYDYSRV
INSP082  QNVLLTHNAEVKLVDGVSQAQVSRNTNGRRNSFIGTPYWMAPEVIDCDEDPRRSYDYSRV
INSP091  QNVLLTHNAEVKLVDGVSQAQVSRNTNGRRNSFIGTPYWMAPEVIDCDEDPRRSYDYSRV
*****

ZC4      WSVGITAIEAEGAPPLCNLQPLEALFVILRESAPTVKSSGWSRKHFHFMKCTIKNFLF
INSP081  WSVGITAIEAEGAPPLCNLQPLEALFVILRESAPTVKSSGWSRKHFHFMKCTIKNFLF
INSP082  WSVGITAIEAEGAPPLCNLQPLEALFVILRESAPTVKSSGWSRKHFHFMKCTIKNFLF
INSP091  WSVGITAIEAEGAPPLCNLQPLEALFVILRESAPTVKSSGWSRKHFHFMKCTIKNFLF
*****

ZC4      RPTSANMLQHPFVRDIKNERHVVESLTRHLTGIIKKRQKK-----→ CP1
INSP081  RPTSANMLQHPFVRDIKNERHVVESLTRHLTGIIKKRQKKGIPLIFEREEAIKEQYTVRR
INSP082  RPTSANMLQHPFVRDIKNERHVVESLTRHLTGIIKKRQKKGIPLIFEREEAIKEQYTVRR
INSP091  RPTSANMLQHPFVRDIKNERHVVESLTRHLTGIIKKRQKKGIPLIFEREEAIKEQYTVRR
*****

ZC4      -----
INSP081  FRGPSCTHELLRLPTSSRCRPLRVLHGEPSPQRWLPDREEPQVQALQQLQGAARVFMPLQ
INSP082  FRGPSCTHELLRLPTSSRCRPLRVLHGEPSPQRWLPDREEPQVQALQQLQGAARVFMPLQ
INSP091  FRGPSCTHELLRLPTSSRCRPLRVLHGEPSPQRWLPDREEPQVQALQQLQGAARVFMPLQ

ZC4      -----
INSP081  ALDSAPKPLKGQAQAPQRLQGAARVFMPLQAQVKAKASKPLQMGIKAPRLRRAARVLMPL
INSP082  ALDSAPKPLKGQAQAPQRLQGAARVFMPLQAQVKAKASKPLQMGIKAPRLRRAARVLMPL
INSP091  ALDSAPKPLKGQAQAPQRLQGAARVFMPLQAQVKAKASKPLQMGIKAPRLRRAARVLMPL
                                     ← CP2

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ZC4
INSP081 LQAQVRAPRLLQVQSQVSKKQQAQTQTSEPQDLDQVPEEFQGGDQVPEQQRQGOAPEQQQ
INSP082 LQAQVRAPRLLQVQSQVSKKQQAQTQTSEPQDLDQVPEEFQGGDQVPEQQRQGOAPEQQQ
INSP091 LQAQVRAPRLLQVQSQVSKKQQAQTQTSEPQDLDQVPEEFQGGDQVPEQQRQGOAPEQQQ

ZC4
INSP081 RHNQVPEQELEQNQAPEQPEVQEQAAPQAETEAEEPESLRVNAQVFLPLLSQDHHVLL
INSP082 RHNQVPEQELEQNQAPEQPEVQEQAAPQAETEAEEPESLRVNAQVFLPLLSQDHHVLL
INSP091 RHNQVPEQELEQNQAPEQPEVQEQAAPQAETEAEEPESLRVNAQVFLPLLSQDHHVLL

ZC4
INSP081 PLHLDQVLIIPVEGQTEGSPQAQAWTLEPPQAIGSVQALIEGLSRDLLRAPNSNNSKPLG
INSP082 PLHLDQVLIIPVEGQTEGSPQAQAWTLEPPQAIGSVQALIEGLSRDLLRAPNSNNSKPLG
INSP091 PLHLDQVLIIPVEGQTEGSPQAQAWTLEPPQAIGSVQALIEGLSRDLLRAPNSNNSKPLG

ZC4
INSP081 -----EQAREKKSKVSTLRQALAKRLSPKRFRAKSSWRPEKLELSDL
INSP082 PLQTLMENLSSNRFYSQPEQAREKKSKVSTLRQALAKRLSPKRFRAKSSWRPEKLELSDL
INSP091 PLQTLMENLSSNRFYSQPEQAREKKSKVSTLRQALAKRLSPKRFRAKSSWRPEKLELSDL

ZC4
INSP081 EARRQRRQRRWEDIFNQHEEELRQVDKDKEDESSDNDEVFHSIQAEVQIEPLKPYISNPK
INSP082 EARRQRRQRRWEDIFNQHEEELRQVDKDKEDESSDNDEVFHSIQAEVQIEPLKPYISNPK
INSP091 EARRQRRQRRWEDIFNQHEEELRQVDKDKEDESSDNDEVFHSIQAEVQIEPLKPYISNPK

ZC4
INSP081 KIEVQERSPSVPNNQDHAHVKFSS-----SVPQRSLLLEQAQKPIDIRQRSSQN
INSP082 KIEVQERSPSVPNNQDHAHVKFSSRTWHMLFCLFISVPQRSLLLEQAQKPIDIRQRSSQN
INSP091 KIEVQERSPSVPNNQDHAHVKFSS-----SVPQRSLLLEQAQKPIDIRQRSSQN

ZC4
INSP081 RQNWLAASGDSKHKILAGKTQSYCLTIYISEVKKEEFQEGMNQKCQGAQVGLGPEGHCW
INSP082 RQNWLAAS-----
INSP091 RQNWLAASGDSKHKILAGKTQSYCLTIYISEVKKEEFQEGMNQKCQGAQVGLGPEGHCW

ZC4
INSP081 QLGEESSEESPVGTGRSSQSSPPYSTIDQKLLVDIHVPDGFVKVGKISPPVYLTNEWVGYN
INSP082 ---ESSEESPVGTGRSSQSSPPYSTIDQKLLVDIHVPDGFVKVGKISPPVYLTNEWVGYN
INSP091 ---ESSEESPVGTGRSSQSSPPYSTIDQKLLVDIHVPDGFVKVGKISPPVYLTNEWVGYN
QLGEESSEESPVGTGRSSQSSPPYSTIDQKLLVDIHVPDGFVKVGKISPPVYLTNEWVGYN

ZC4
INSP081 ALSEIFRNDWLTAPVVIQPPPEEDGDYVELYDASADTDGDDDDDESNDTFEDTYDHANGND
INSP082 ALSEIFRNDWLTAPVVIQPPPEEDGDYVELYDASADTDGDDDDDESNDTFEDTYDHANGND
INSP091 ALSEIFRNDWLTAPVVIQPPPEEDGDYVELYDASADTDGDDDDDESNDTFEDTYDHANGND

ZC4
INSP081 LDNQVDQANDVCKDHDDNNKFVDDVNNNYYEAPSCPRASYGRDGSKQDGYDGSRGKEE
INSP082 LDNQVDQANDVCKDHDDNNKFVDDVNNNYYEAPSCPRASYGRDGSKQDGYDGSRGKEE
INSP091 LDNQVDQANDVCKDHDDNNKFVDDVNNNYYEAPSCPRASYGRDGSKQDGYDGSRGKEE

ZC4
INSP081 AYRGYGSHTANRSHGGSAASEDNAAIGDQEEHAANIGSERRGSEGDDGGKGVVRTSEESGA
INSP082 AYRGYGSHTANRSHGGSAASEDNAAIGDQEEHAANIGSERRGSEGDDG-----
INSP091 AYRGYGSHTANRSHGGSAASEDNAAIGDQEEHAANIGSERRGSEGDDG-----

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ZC4 LGLNGEENCSETDGPGLKR PASQDFEYLQEEP GGGNEASNAIDSGAAPSAPDHESDNKDI
INSP081 -----GGNEASNAIDSGAAPSAPDHESDNKDI
INSP082 -----GGNEASNAIDSGAAPSAPDHESDNKDI
INSP091 LGLNGEENCSETDGPGLKR PASQDFEYLQEEP GGGNEASNAIDSGAAPSAPDHESDNKDI

ZC4 SESSTQSDFSANHSSPSKSGSGMSADANFASAILYAGFVEVPEESPKQPSEVNVNPLYVSP
INSP081 SESSTQSDFSANHSSPSKSGSGMSADANFASAI-----
INSP082 SESSTQSDFSANHSSPSKSGSGMSADANFASAILYAGFVEVPEESPKQPSEVNVNPLYVSP
INSP091 SESSTQSDFSANHSSPSKSGSGMSADANFASAILYAGFVEVPEESPKQPSEVNVNPLYVSP

ZC4 ACKKPLIHMYEKEFTSEICCGSLWGVNLLLGTNRNLYLMDRSGKADITKLIRRRPFRQIQ
INSP081 -----
INSP082 ACKKPLIHMYEKEFTSEICCGSLWGVNLLLGTNRNLYLMDRSGKADITKLIRRRPFRQIQ
INSP091 ACKKPLIHMYEKEFTSEICCGSLWGVNLLLGTNRNLYLMDRSGKADITKLIRRRPFRQIQ

ZC4 VLEPLNLLITISGHKNRLRVYHLTWLRNKILNNDPESKRRQEEMLKTEEACKAIDKLTGC
INSP081 -----
INSP082 VLEPLNLLITISGHKNRLRVYHLTWLRNKILNNDPESKRRQEEMLKTEEACKAIDKLTGC
INSP091 VLEPLNLLITISGHKNRLRVYHLTWLRNKILNNDPESKRRQEEMLKTEEACKAIDKLTGC

ZC4 EHFSVLQHEETTYIAIALKSSIHLYAWAPKSFDESTAIKVFPPTLDHKPVTVDLAIGSEKR
INSP081 -----
INSP082 EHFSVLQHEETTYIAIALKSSIHLYAWAPKSFDESTAIKVFPPTLDHKPVTVDLAIGSEKR
INSP091 EHFSVLQHEETTYIAIALKSSIHLYAWAPKSFDESTAIKVFPPTLDHKPVTVDLAIGSEKR

ZC4 LKIFFSSADGYHLIDAESEVMSDVTL PKNPLEIIIPQNIILPDCLGIGMMLTFNAEALS
INSP081 -----
INSP082 LKIFFSSADGYHLIDAESEVMSDVTL PKNPLEIIIPQNIILPDCLGIGMMLTFNAEALS
INSP091 LKIFFSSADGYHLIDAESEVMSDVTL PKNPLEIIIPQNIILPDCLGIGMMLTFNAEALS

ZC4 VEANEQLFKKILEMWKDIPSSIAFECTQRTTGWGQKAIEVRSLQSRVLESELKRRSIKKL
INSP081 -----
INSP082 VEANEQLFKKILEMWKDIPSSIAFECTQRTTGWGQKAIEVRSLQSRVLESELKRRSIKKL
INSP091 VEANEQLFKKILEMWKDIPSSIAFECTQRTTGWGQKAIEVRSLQSRVLESELKRRSIKKL

ZC4 RFLCTRGDKLFFTSTLRNHHSRVYFMTLGKLEELQSNYDV
INSP081 -----
INSP082 RFLCTRGDKLFFTSTLRNHHSRVYFMTLGKLEELQSNYDV
INSP091 RFLCTRGDKLFFTSTLRNHHSRVYFMTLGKLEELQSNYDV

Figure 8: Nucleotide sequence with translation of INSP082 PCR product cloned using primers INSP082-CP1 and INSP082-CP2.

```

1  aggaacagta caccgtgaga agattcagag gaccctcttg cactcacgag cttctgagat
    INSP082-CP1
    e q y t v r r f r g p s c t h e l l r

61  tgccaaccag cagcagatgc agaccactta gagtcctgca tggggaaccc tctcagccaa
    l p t s s r c r p l r v l h g e p s q p

121  ggtggctacc tgatcgagaa gagccacagg tccaggcact tcagcagcta cagggagcag
    r w l p d r e e p q v q a l q q l q g a

181  ccaggggtatt catgccactg caggctctgg acagtgcacc taagcctcta aaggggcagg
    a r v f m p l q a l d s a p k p l k g q

241  ctcaggcacc tcaacgacta caaggggcag ctcgggtggt catgccacta caggctcagg
    a q a p q r l q g a a r v f m p l q a q

301  tgaaggctaa agcctctaaa cctctacaaa tgcagattaa ggcacctcca cgact
    v k a k a s k p l q m q i k a p p r
    INSP082-CP2

```

Position and sense of PCR primers →

Figure 9: Nucleotide sequence with translation of INSP082 PCR product cloned using primers INSP082-CP3 and INSP082-CP4.

```

1  taggaaggcg agtgagagtg aataaatatc aaaaatctgt tgggtggaga tacagtgatg
    INSP082-CP3
    g r r v r v n k y q k s v g w r y s d

61  aggaagagga tctcaggact gaactcaacc ttctgaggaa gtactctttc cacaaaaaca
    e e e d l r t e l n l l r k y s f h k n

121 ttgtgtcctt ctatggagca tttttcaagc tgagtcccc tggtcagcgg caccaacttt
    i v s f y g a f f k l s p p g q r h q l

181 ggatggtgat ggagttatgt gcagcagggt cggtcactga tgtagtgaga atgaccagta
    w m v m e l c a a g s v t d v v r m t s

241 atcagagttt aaaagaagat tggattgctt atatctgccg agaaatcctt cagggttag
    n q s l k e d w i a y i c r e i l q g l

301 ctcaccttca cgcacaccga gtaattcacc gg
    INSP082-CP4
    a h l h a h r v i h r
  
```

Position and sense of PCR primers 